P.O #8

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/744,085

DATE: 07/15/2001
TIME: 20:07:33

Input Set : A:\744085seq.jun.txt
Output Set: N:\CRF3\07152001\I744085.raw

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 3 <110> APPLICANT: Schaffer, Arthur
 4          Levin, Ilan
 5          Petreikov, Marina
 6          Bar, Moshe
 8 <120> TITLE OF INVENTION: Controlling Starch Synthesis
10 <130> FILE REFERENCE: U-013220-5
12 <140> CURRENT APPLICATION NUMBER: US 09/744,085
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C--> `13 <141> CURRENT FILING DATE: 2001-06-21`
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15 <150> PRIOR APPLICATION NUMBER: PCT/IL99/00396
16 <151> PRIOR FILING DATE: 1999-07-19
18 <150> PRIOR APPLICATION NUMBER: IL 125425
19 <151> PRIOR FILING DATE: 1998-07-20
21 <160> NUMBER OF SEQ ID NOS: 10
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 23
27 <212> TYPE: DNA
28 <213> ORGANISM: Lycopersicon hirsutum
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35 <211> LENGTH: 23
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71 <211> LENGTH: 22
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76  cttttcgctg aaggacatga cc                                        22
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80  <211> LENGTH: 23
81  <212> TYPE: DNA
82  <213> ORGANISM: Lycopersicon hirsutum
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85  tttcgtcttc tcatctcgcc gga                                       23
88  <210> SEQ ID NO: 8
89  <211> LENGTH: 23
90  <212> TYPE: DNA
91  <213> ORGANISM: Lycopersicon hirsutum
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94  ggcgatttag agaggcagag ttg                                       23
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98  <211> LENGTH: 1563
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100 <213> ORGANISM: Lycopersicon hirsutum
102 <220> FEATURE:
103 <221> NAME/KEY: CDS
104 <222> LOCATION: (1)..(1563)
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109  1               5                  10                  15
111 aat gga gag aag gag att ttt ggg gag aag atg aga ggg agt ttg aac    96
112 Asn Gly Glu Lys Glu Ile Phe Gly Glu Lys Met Arg Gly Ser Leu Asn
113              20                  25                  30
115 aac aat ctc agg att aat cag ttg tcg aaa agt ttg aaa ctt gag aag   144
116 Asn Asn Leu Arg Ile Asn Gln Leu Ser Lys Ser Leu Lys Leu Glu Lys
117          35                  40                  45
119 aag gag aag aag att aaa cct ggg gtt gct tac tct gtg atc act act   192
120 Lys Glu Lys Lys Ile Lys Pro Gly Val Ala Tyr Ser Val Ile Thr Thr
121      50                  55                  60
123 gaa aat gac aca gag act gtg ttc gta gat atg cca cgt ctt gag aga   240
124 Glu Asn Asp Thr Glu Thr Val Phe Val Asp Met Pro Arg Leu Glu Arg
125  65                  70                  75                  80
127 cgc cgg gca aat ccc aag gat gtg gct gca gtc ata tta gga gga ggc   288
128 Arg Arg Ala Asn Pro Lys Asp Val Ala Ala Val Ile Leu Gly Gly Gly
129              85                  90                  95
131 gaa ggg acc aag tta ttc cca ctt aca agt aga act gca acc cct gct   336
132 Glu Gly Thr Lys Leu Phe Pro Leu Thr Ser Arg Thr Ala Thr Pro Ala
133             100                 105                 110
135 gtt ccg gtt gga gga tgc tac agg ctc ata gac atc ccg atg agc aac   384
136 Val Pro Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn
137         115                 120                 125
139 tgt atc aac agt gct att aac aag att ttt gtg ctg aca cag tac aat   432
140 Cys Ile Asn Ser Ala Ile Asn Lys Ile Phe Val Leu Thr Gln Tyr Asn
```

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141       130                         135                        140
143 tct gct gcc ctg aat cgt cac att gct cga acg tat ttt ggc aat ggt    480
144 Ser Ala Ala Leu Asn Arg His Ile Ala Arg Thr Tyr Phe Gly Asn Gly
145 145                         150                        155                        160
147 gtg agc ttt gga gat gga ttt gtc gag gta cta gct gca act cag aca    528
148 Val Ser Phe Gly Asp Gly Phe Val Glu Val Leu Ala Ala Thr Gln Thr
149                         165                        170                        175
151 cct ggg gaa gca gga aaa aaa tgg ttt caa gga aca gca gat gct gtc    576
152 Pro Gly Glu Ala Gly Lys Lys Trp Phe Gln Gly Thr Ala Asp Ala Val
153                         180                        185                        190
155 aga aaa ttt ata tgg gtt ttt gag gac gct aag aac aag aat att gaa    624
156 Arg Lys Phe Ile Trp Val Phe Glu Asp Ala Lys Asn Lys Asn Ile Glu
157           195                        200                        205
159 aat atc ctt gta tta tct ggg gat cat ctt tat agg atg gat tat atg    672
160 Asn Ile Leu Val Leu Ser Gly Asp His Leu Tyr Arg Met Asp Tyr Met
161       210                         215                        220
163 gag ttg gtg cag aac cat att gac aga aat gct gat att act ctt tca    720
164 Glu Leu Val Gln Asn His Ile Asp Arg Asn Ala Asp Ile Thr Leu Ser
165 225                         230                        235                        240
167 tgt gca cca gct gag gac agc cga gca tca gat ttt ggg ctg gtc aag    768
168 Cys Ala Pro Ala Glu Asp Ser Arg Ala Ser Asp Phe Gly Leu Val Lys
169                         245                        250                        255
171 att gac agc aga ggc aga gtt gtc cag ttt gct gaa aaa cca aaa ggt    816
172 Ile Asp Ser Arg Gly Arg Val Val Gln Phe Ala Glu Lys Pro Lys Gly
173           260                        265                        270
175 ttt gag ctt aaa gca atg caa gta gat act act ctt gtt gga tta tct    864
176 Phe Glu Leu Lys Ala Met Gln Val Asp Thr Thr Leu Val Gly Leu Ser
177           275                        280                        285
179 cca caa gat gcg aag aaa tcc cct tat att gct tca atg gga gtt tat    912
180 Pro Gln Asp Ala Lys Lys Ser Pro Tyr Ile Ala Ser Met Gly Val Tyr
181       290                         295                        300
183 gtt ttc aag aca gat gta ttg ctg aag ctc ttg aaa tgg agc tac ccc    960
184 Val Phe Lys Thr Asp Val Leu Leu Lys Leu Leu Lys Trp Ser Tyr Pro
185 305                         310                        315                        320
187 act tct aat gat ttt ggc tct gaa att ata cca gca gct att gat gat    1008
188 Thr Ser Asn Asp Phe Gly Ser Glu Ile Ile Pro Ala Ala Ile Asp Asp
189                         325                        330                        335
191 tac aat gtc caa gca tac att ttc aaa gac tat tgg gag gac att gga    1056
192 Tyr Asn Val Gln Ala Tyr Ile Phe Lys Asp Tyr Trp Glu Asp Ile Gly
193                         340                        345                        350
195 aca att aaa tct ttc tat aat gct agc ttg gcg ctc aca caa gag ttt    1104
196 Thr Ile Lys Ser Phe Tyr Asn Ala Ser Leu Ala Leu Thr Gln Glu Phe
197           355                        360                        365
199 cca gag ttc caa ttt tat gat cca aaa aca cct ttt tac aca tct cct    1152
200 Pro Glu Phe Gln Phe Tyr Asp Pro Lys Thr Pro Phe Tyr Thr Ser Pro
201       370                         375                        380
203 agg ttc ctt cca cca acc aag ata gac aat tgc aag att aag gat gcc    1200
204 Arg Phe Leu Pro Pro Thr Lys Ile Asp Asn Cys Lys Ile Lys Asp Ala
205 385                         390                        395                        400
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207 ata att tct cat gga tgt ttc ttg cga gat tgc tct gtg gaa cac tcc   1248
208 Ile Ile Ser His Gly Cys Phe Leu Arg Asp Cys Ser Val Glu His Ser
209             405                 410                 415
211 ata gtg ggt gaa aga tca cgc tta gac tgt ggt gtt gaa ctg aag gat   1296
212 Ile Val Gly Glu Arg Ser Arg Leu Asp Cys Gly Val Glu Leu Lys Asp
213             420                 425                 430
215 act ttc atg atg gga gca gac tac tac caa aca gaa tct gag att gcc   1344
216 Thr Phe Met Met Gly Ala Asp Tyr Tyr Gln Thr Glu Ser Glu Ile Ala
217             435                 440                 445
219 tcc ctg tta gca gag ggg aaa gta ccg att ggg att ggg gaa aat aca   1392
220 Ser Leu Leu Ala Glu Gly Lys Val Pro Ile Gly Ile Gly Glu Asn Thr
221     450                 455                 460
223 aaa ata agg aaa tgt atc att gac aag aac gca aag ata gga aaa aat   1440
224 Lys Ile Arg Lys Cys Ile Ile Asp Lys Asn Ala Lys Ile Gly Lys Asn
225 465                 470                 475                 480
227 gtt tca atc att aat aaa gat ggt gtt caa gag gca gac cga cca gag   1488
228 Val Ser Ile Ile Asn Lys Asp Gly Val Gln Glu Ala Asp Arg Pro Glu
229                 485                 490                 495
231 gaa gga ttc tac ata cga tca ggg ata acc att ata tca gag aaa gcc   1536
232 Glu Gly Phe Tyr Ile Arg Ser Gly Ile Thr Ile Ile Ser Glu Lys Ala
233             500                 505                 510
235 aca att aga gat gga aca gtt ata tga                               1563
236 Thr Ile Arg Asp Gly Thr Val Ile
237         515                 520
240 <210> SEQ ID NO: 10
241 <211> LENGTH: 520
242 <212> TYPE: PRT
243 <213> ORGANISM: Lycopersicon hirsutum
245 <400> SEQUENCE: 10
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250             20                  25                  30
252 Asn Asn Leu Arg Ile Asn Gln Leu Ser Lys Ser Leu Lys Leu Glu Lys
253             35                  40                  45
255 Lys Glu Lys Lys Ile Lys Pro Gly Val Ala Tyr Ser Val Ile Thr Thr
256     50                  55                  60
258 Glu Asn Asp Thr Glu Thr Val Phe Val Asp Met Pro Arg Leu Glu Arg
259 65                  70                  75                  80
261 Arg Arg Ala Asn Pro Lys Asp Val Ala Ala Val Ile Leu Gly Gly Gly
262             85                  90                  95
264 Glu Gly Thr Lys Leu Phe Pro Leu Thr Ser Arg Thr Ala Thr Pro Ala
265             100                 105                 110
267 Val Pro Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn
268     115                 120                 125
270 Cys Ile Asn Ser Ala Ile Asn Lys Ile Phe Val Leu Thr Gln Tyr Asn
271     130                 135                 140
273 Ser Ala Ala Leu Asn Arg His Ile Ala Arg Thr Tyr Phe Gly Asn Gly
274 145                 150                 155                 160
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276 Val Ser Phe Gly Asp Gly Phe Val Glu Val Leu Ala Ala Thr Gln Thr
277          165              170              175
279 Pro Gly Glu Ala Gly Lys Lys Trp Phe Gln Gly Thr Ala Asp Ala Val
280          180              185              190
282 Arg Lys Phe Ile Trp Val Phe Glu Asp Ala Lys Asn Lys Asn Ile Glu
283          195              200              205
285 Asn Ile Leu Val Leu Ser Gly Asp His Leu Tyr Arg Met Asp Tyr Met
286     210              215              220
288 Glu Leu Val Gln Asn His Ile Asp Arg Asn Ala Asp Ile Thr Leu Ser
289 225              230              235              240
291 Cys Ala Pro Ala Glu Asp Ser Arg Ala Ser Asp Phe Gly Leu Val Lys
292          245              250              255
294 Ile Asp Ser Arg Gly Arg Val Val Gln Phe Ala Glu Lys Pro Lys Gly
295          260              265              270
297 Phe Glu Leu Lys Ala Met Gln Val Asp Thr Thr Leu Val Gly Leu Ser
298          275              280              285
300 Pro Gln Asp Ala Lys Lys Ser Pro Tyr Ile Ala Ser Met Gly Val Tyr
301     290              295              300
303 Val Phe Lys Thr Asp Val Leu Leu Lys Leu Leu Lys Trp Ser Tyr Pro
304 305              310              315              320
306 Thr Ser Asn Asp Phe Gly Ser Glu Ile Ile Pro Ala Ala Ile Asp Asp
307          325              330              335
309 Tyr Asn Val Gln Ala Tyr Ile Phe Lys Asp Tyr Trp Glu Asp Ile Gly
310          340              345              350
312 Thr Ile Lys Ser Phe Tyr Asn Ala Ser Leu Ala Leu Thr Gln Glu Phe
313          355              360              365
315 Pro Glu Phe Gln Phe Tyr Asp Pro Lys Thr Pro Phe Tyr Thr Ser Pro
316     370              375              380
318 Arg Phe Leu Pro Pro Thr Lys Ile Asp Asn Cys Lys Ile Lys Asp Ala
319 385              390              395              400
321 Ile Ile Ser His Gly Cys Phe Leu Arg Asp Cys Ser Val Glu His Ser
322          405              410              415
324 Ile Val Gly Glu Arg Ser Arg Leu Asp Cys Gly Val Glu Leu Lys Asp
325          420              425              430
327 Thr Phe Met Met Gly Ala Asp Tyr Tyr Gln Thr Glu Ser Glu Ile Ala
328          435              440              445
330 Ser Leu Leu Ala Glu Gly Lys Val Pro Ile Gly Ile Gly Glu Asn Thr
331     450              455              460
333 Lys Ile Arg Lys Cys Ile Ile Asp Lys Asn Ala Lys Ile Gly Lys Asn
334 465              470              475              480
336 Val Ser Ile Ile Asn Lys Asp Gly Val Gln Glu Ala Asp Arg Pro Glu
337          485              490              495
339 Glu Gly Phe Tyr Ile Arg Ser Gly Ile Thr Ile Ile Ser Glu Lys Ala
340          500              505              510
342 Thr Ile Arg Asp Gly Thr Val Ile
343     515              520
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